

RAW SEQUENCE LISTING PATENT APPLICATION US/08/972,301

DATE: 12/28/1999 TIME: 00:28:00

INPUT SET: S34317.raw

This Raw Listing contains the General Information Section and up to the first pages. TERFO

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1
                                        SEQUENCE LISTING
 2
     (1)
 3
            General Information:
 4
 5
          (i) APPLICANT: Coleman, Timothy A.
 6
                          Rosen, Craig A.
 7
 8
         (ii) TITLE OF INVENTION: Endothelial Monocyte Activating
 9
                 Polypeptide III
10
11
        (iii) NUMBER OF SEQUENCES: 7
12
13
         (iv) CORRESPONDENCE ADDRESS:
14
                (A) ADDRESSEE: Human Genome Sciences, Inc.
                (B) STREET: 9410 Key West Avenue
15
16
                (C) CITY: Rockville,
               (D) STATE: MD
17
18
               (E) COUNTRY: USA
19
               (F) ZIP: 20850
20
21
          (v) COMPUTER READABLE FORM:
               (A) MEDIUM TYPE: Floppy disk
               (B) COMPUTER: IBM PC compatible
               (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25
               (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
26
         (vi) CURRENT APPLICATION DATA:
27
28
               (A) APPLICATION NUMBER: US 08/972,301
29
               (B) FILING DATE: 18-NOV-1997
               (C) CLASSIFICATION:
30
31
        (vii) PRIOR APPLICATION DATA:
32
33
               (A) APPLICATION NUMBER: US 08/483,534
34
               (B) FILING DATE: 07-JUN-1995
35
36
       (viii) ATTORNEY/AGENT INFORMATION:
37
               (A) NAME: Marks, Michelle S.
38
               (B) REGISTRATION NUMBER: 41,971
39
               (C) REFERENCE/DOCKET NUMBER: PF206D1
40
41
         (ix) TELECOMMUNICATION INFORMATION:
42
               (A) TELEPHONE: 301-309-8504
43
               (B) TELEFAX: 301-309-8439
44
45
46
     (2) INFORMATION FOR SEQ ID NO:1:
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														41	** **	DEL. D.	3 .01 · a ··
47 48 49 50 51 52		(i)	() () ()	A) L B) T C) S	ENGT: YPE : TRAN	HARA H: 6: nuc: DEDN:	36 b leic ESS:	ase ; aci sin	pair d	s							
53 54 55 56		(ii)) MO	LECU	LE T	YPE:	DNA	(ge:	nomi	c)							
57 58 59 60	(ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 94597																
62 63	•																
64 65																	
66 67 68 69	AATG	GCC <i>I</i>	AAA (GCC'	TGCC	AA G	TTAA	CAGA	A CC	Gl				e Pr		c cgg r Arg	114
70 71 72 73	CTG (162
74 75 76 77	GCA (210
78 79 80 81	CGG A Arg 5																258
82 83 84 85	CAG (306
86 87 88 89	AGA (Leu							354
90 91 92 93	ATA A																. 402
94 95 96 97	GGT (450
98 99	GAG (498

RAW SEQUENCE LISTING PATENT APPLICATION US/08/972,301

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100 101	120					125					130					135	
102	AAA	ATT	TCT	GAG	GAG	TGC	ATC	GCA	CAG	TGG	AAG	CAA	ACC	AAC	TTC	ATG	546
103	Lys	Ile	Ser	Glu	Glu	Cys	Ile	Ala	Gln	Trp	Lys	Gln	Thr	Asn	Phe	Met	
104					140					145					150		
105	•																
106				GGC													594
107	Thr	Lys	Leu	Gly	Ser	Ile	Ser	Cys	-	Ser	Leu	Lys	Gly	_	Asn	Ile	
108				155					160					165			
109																	
110		TAG	CCAG	CCC 2	AGCA'	rctt(CC C	CCCT"	rctt(C CA	CCAC'	TGA					636
111	Ser																
112																	
113																	
114	(2)	TATE	OD8431	m T O N	EOD	O E O	TD 1	TO - 0	_							·	
115 116	(2)	TNE	JRMA	TION	FOR	SEQ	ו עד	NO: 2	:								
117	(1) GEOLUTIAN GUADAGMED TOMTOG																
117	(i) SEQUENCE CHARACTERISTICS:																
119	(A) LENGTH: 168 amino acids (B) TYPE: amino acid																
120	(D) TOPOLOGY: linear																
121	• •																
122		(:	ii) 1	MOLE	CULE	TYPI	E: p:	rote	in								
123		•	, .				-· P·										
124		(:	xi) :	SEQUI	ENCE	DES	CRIP'	TION	: SEC	O ID	NO:2	2:					
125		·	•	_					•	-	-						
126	Glu	Glu	Val	Ile	Pro	Ser	Arg	Leu	Asp	Ile	Arg	Val	Gly	Lys	Ile	Ile	
127	1				5		•		-	10	_		-	-	15		
128																	
129	Thr	Val	Glu	Lys	His	Pro	Asp	Ala	Asp	Ser	Leu	Tyr	Val	Glu	Lys	Ile	
130				20					25					30			
131																	
132	Asp	Val	Gly	Glu	Ala	Glu	Pro	Arg	Thr	Val	Val	Ser	Gly	Leu	Val	Gln	
133			35					40					45				
134								_				_	_	_			
135	Phe		Pro	Lys	Glu	Glu		Gln	Asp	Arg	Leu		Val	Val	Leu	Cys	
136		50					55					60					
137	3	•	•	5	~ 7	•	37 - 4-		~ 1	7	~1		~1	~1		•	
138		ьeu	гуѕ	Pro	Gin	_	Met	Arg	GIA	vaı		Ser	GIn	GLY	Met		
139	65					70					75					80	
140 141	T 011	Crea	77-	002	т1.	~1	~1	т1.	2 an	7 ~~	@1 m	170.1	~1	Dwo	T 011	A am	
141	Leu	Cys	Ата	Ser	85	GIU	GIY	TTE	ASII	90	GIII	val	GIU	PIO	95	Asp	
143					05					90					93		
144	Pro	Pro	Δla	Gly	Ser	Δla	Pro	Glv	Glu	His	Va 1	Phe	Val	Lvs	Glv	Tur	
145	-10			100	JUL		110	- Ly	105		VUL	1110	741	110	- Y	-1-	
146																	
147	Glu	Lys	Glv	Gln	Pro	Asp	Glu	Glu	Leu	Lys	Pro	Lvs	Lys	Lys	Val	Phe	
148			115					120		. -		4 -	125	4			
149																	
150	Glu	Lys	Leu	Gln	Ala	Asp	Phe	Lys	Ile	Ser	Glu	Glu	Cys	Ile	Ala	Gln	
151		130				_	135					140					
152																	

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DATE: 12/28/1999 TIME: 00:28:01

INPUT SET: S34317.raw Trp Lys Gln Thr Asn Phe Met Thr Lys Leu Gly Ser Ile Ser Cys Lys Ser Leu Lys Gly Gly Asn Ile Ser (2) INFORMATION FOR SEQ ID NO:3: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 28 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3: GATCGGATCC GAGGAGGTCA TCCCATCC (2) INFORMATION FOR SEQ ID NO:4: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 28 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4: GATCAAGCTT CTAGATAATG TTCCCCCC (2) INFORMATION FOR SEQ ID NO:5: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 28 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic)

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206	(xi)	SEQ	UENC	E DE	SCRI	PTIO	N: S	EQ I	D NO	:5:							
207																	
208	GATCGGATCC GAGGAGGTCA TCCCATCC 28														28		
209																	
210	(2) INFORMATION FOR SEQ ID NO:6:																
211																	
212	(i)	SEQ															
213						bas	_										
214		-	-			eic .											
215						SS:		le									
216		(D) TO	POLO	GY:	line	ar										
217																	
218	(ii)	MOL	ECUL.	E TY	PE:	DNA	(gen	omic)								
219																	
220																	
221																	
222																	
223	(xi)	SEQ	UENC	E DE	SCRI	PTIO	N: S	EQ I	D NO	:6:							
224																	
225	GATCGGAT	CC C	TAGA'	TAAT	G TT	CCCC	CC										28
226	(0)																
227	(2) INFO	RMAT	ION .	FOR :	SEQ	ID N	0:7:										
228																	
229	(i) SEQUENCE CHARACTERISTICS:																
230	(A) LENGTH: 183 amino acids																
231	(B) TYPE: amino acid																
232	(C) STRANDEDNESS: single																
233	(D) TOPOLOGY: linear																
234 235	(ii) MOLECULE TYPE: protein																
235 236	(11)	MOT.	RCOT!	E TY	PE:]	prot	eın										
236																	
237																	
239																	
240	(vi)	SEQ	TENC	ישרו יש	COT	וחדיים	M. C'	E0 T1	D NO	. 7 .							
241	(XI)	DEQ	0131401	,حال ت	JCKI.	F 1 1 0.	и. Б.	EQ I	D NO	• / •							
242	Lvg	Glv	Glu	Lvg	Lvg	Glu	Lve	Taye	Gln	G]n	Ser	Tle	Δla	Glv	Ser	Δla	
243	1	017	Ų1u	_,	5	Olu	Lys	Lys	0111	10	DCI	110	AIu	Cry	15	AIG	
244	-				-					10					13		
245	Asp	Ser	Lvs	Pro	Tle	Asn	Val	Ser	Ara	Leu	Asp	Leu	Ara	Tle	Gly	Cvs	
246			_,_												_	.07.0	
247														•			
248	Ile	Ile	Thr	Ala	Ara	Lvs	His	Pro	Asp	Ala	Asp	Ser	Leu	Tvr	Val	Glu	
249			35		5	-1-		40			<u>-</u>		45	-1-			
250																	
251	Glu	Val	asa	Val	Glv	Glu	Ile	Ala	Pro	Ara	Thr	Val	Val	Ser	Gly	Leu	
252		50			1		55			د		60			1		
253		-															
254	Val	Asn	His	Val	Pro	Leu	Glu	Gln	Met	Gln	Asn	Ara	Met	Val	Ile	Leu	
255	65	-		_	_	70			_		75	ر	_			80	
256																	*
257	Leu	Cys	Asn	Leu	Lys	Pro	Ala	Lys	Met	Arg	Gly	Val	Lys	Ser	Gln	Ala	
258		-			85			-		90	-		-		95		

SEQUENCE VERIFICATION REPORT PATENT APPLICATION US/08/972,301

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